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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Wed Aug 08 14:07:27 EDT 2007

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Reviewer Comments:

<160> 13

Although the above <160> response is "13," 18 sequences are shown in the submitted file. See below:

<210> 18

<211> 225

<212> PRT

<213> Mus musculus

<400> 18

Met Leu Leu Thr Leu Ala Gly Gly Ala Leu Phe Phe Pro Gly Leu Phe

(the above is a sample of Sequence 18, the last sequence in the file)

Application No: 10536772 Version No: 2.0

Input Set:

Output Set:

Started: 2007-08-06 11:18:39.445
Finished: 2007-08-06 11:18:41.545
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 100 ms
Total Warnings: 11
Total Errors: 13
No. of SeqIDs Defined: 13
Actual SeqID Count: 18

Error code	Error Description
E 201	Mandatory field data missing in <223> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)

Input Set:

Output Set:

Started: 2007-08-06 11:18:39.445
Finished: 2007-08-06 11:18:41.545
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 100 ms
Total Warnings: 11
Total Errors: 13
No. of SeqIDs Defined: 13
Actual SeqID Count: 18

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
E 252	Calc# of Seq. differs from actual; 13 seqIds defined; count=18

Sequence listing

<110> SHANGHAI CANCER INSTITUTE

<120> A HUMAN TUMOR-ASSOCIATED GENE CT120 ON CHROMOSOME 17P 13.3 REGION AND PROTEIN ENCODED BY IT

<130> 024832pc

<140> 10536772

<141> 2005-05-26

<150>

<151>

<150> CN 02150730.9

<151> 2002-11-27

<160> 13

<170> PatentIn version 3.1

<210> 1

<211> 2145

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(861)

<223>

<400> 1

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cggagggttg aaatcgcgcg gccggggccgg ggcgcgcgcga gccgaaccca gccacgcggc      60
gccagcgagg cggccggacc cgcagccccc atg ctg ctg acg ctg gcc ggg ggc      114
                               Met Leu Leu Thr Leu Ala Gly Gly
                               1             5
gcg ctc ttc ttc ccg ggg ctc ttc gcg ctc tgc acc tgg gcg ctg cgc      162
Ala Leu Phe Phe Pro Gly Leu Phe Ala Leu Cys Thr Trp Ala Leu Arg
   10             15             20
cac tcc cag ccc gga tgg agc cgc acc gac tgc gtg atg atc agc acc      210
His Ser Gln Pro Gly Trp Ser Arg Thr Asp Cys Val Met Ile Ser Thr
   25             30             35             40
agg ctg gtt tcc tcg gtg cac gcc gtg ctg gcc acc ggc tcg ggg atc      258
Arg Leu Val Ser Ser Val His Ala Val Leu Ala Thr Gly Ser Gly Ile
           45             50             55
gtc atc att cgc tcc tgc gac gac gtg atc acc ggc agg cac tgg ctt      306
Val Ile Ile Arg Ser Cys Asp Asp Val Ile Thr Gly Arg His Trp Leu
           60             65             70
gcc cgg gaa tat gtg tgg ttt ctg att cca tac atg atc tat gac tcg      354
Ala Arg Glu Tyr Val Trp Phe Leu Ile Pro Tyr Met Ile Tyr Asp Ser
           75             80             85
tac gcc atg tac ctc tgt gaa tgg tgc cga acc aga gac cag aac cgt      402
Tyr Ala Met Tyr Leu Cys Glu Trp Cys Arg Thr Arg Asp Gln Asn Arg
           90             95            100
gcg ccc tcc ctc act ctt cga aac ttc cta agt cga aac cgc ctc atg      450

```

[illegible]

<400> 2

Met	Leu	Leu	Thr	Leu	Ala	Gly	Gly	Ala	Leu	Phe	Phe	Pro	Gly	Leu	Phe
1				5					10					15	
Ala	Leu	Cys	Thr	Trp	Ala	Leu	Arg	His	Ser	Gln	Pro	Gly	Trp	Ser	Arg
			20					25					30		
Thr	Asp	Cys	Val	Met	Ile	Ser	Thr	Arg	Leu	Val	Ser	Ser	Val	His	Ala
		35					40					45			
Val	Leu	Ala	Thr	Gly	Ser	Gly	Ile	Val	Ile	Ile	Arg	Ser	Cys	Asp	Asp
	50					55					60				
Val	Ile	Thr	Gly	Arg	His	Trp	Leu	Ala	Arg	Glu	Tyr	Val	Trp	Phe	Leu
65					70					75					80
Ile	Pro	Tyr	Met	Ile	Tyr	Asp	Ser	Tyr	Ala	Met	Tyr	Leu	Cys	Glu	Trp
				85					90					95	
Cys	Arg	Thr	Arg	Asp	Gln	Asn	Arg	Ala	Pro	Ser	Leu	Thr	Leu	Arg	Asn
			100					105					110		
Phe	Leu	Ser	Arg	Asn	Arg	Leu	Met	Ile	Thr	His	His	Ala	Val	Ile	Leu
		115					120					125			
Leu	Val	Leu	Val	Pro	Val	Ala	Gln	Arg	Leu	Arg	Gly	Asp	Leu	Gly	Asp
	130					135					140				
Phe	Phe	Val	Gly	Cys	Ile	Phe	Thr	Ala	Glu	Leu	Ser	Thr	Pro	Phe	Val
145					150					155					160
Ser	Leu	Gly	Arg	Val	Leu	Ile	Gln	Leu	Lys	Gln	Gln	His	Thr	Leu	Leu
			165					170						175	
Tyr	Lys	Val	Asn	Gly	Ile	Leu	Thr	Leu	Ala	Thr	Phe	Leu	Ser	Cys	Arg
			180					185					190		
Ile	Leu	Leu	Phe	Pro	Phe	Met	Tyr	Trp	Ser	Tyr	Gly	Arg	Gln	Gln	Gly
	195					200					205				
Leu	Ser	Leu	Leu	Gln	Val	Pro	Phe	Ser	Ile	Pro	Phe	Tyr	Cys	Asn	Val
	210					215					220				
Ala	Asn	Ala	Phe	Leu	Val	Ala	Pro	Gln	Ile	Tyr	Trp	Phe	Cys	Leu	Leu
225					230					235					240
Cys	Arg	Lys	Ala	Val	Arg	Leu	Phe	Asp	Thr	Pro	Gln	Ala	Lys	Lys	Asp
			245					250						255	

Gly

<210> 3
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> misc_feature
 <222> (1)..(25)
 <223> primer

<400> 3
 gtgcgactgg cacaaggaca aagag

25

<210> 4
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> misc_feature
 <222> (1)..(23)

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<223> primer

<400> 4
cgaatgatga cgatccccga gcc 23

<210> 5
<211> 22
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(22)
<223> primer

<400> 5
ccgatgctgc tgacgctggc cg 22

<210> 6
<211> 25
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(25)
<223> primer

<400> 6
tgttggcacc agaaaatcct gcttg 25

<210> 7
<211> 20
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(20)
<223> primer

<400> 7
aagtactccg tgtggatcgg 20

<210> 8
<211> 20
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(20)
<223> primer

<400> 8
tcaagttggg ggacaaaaag 20

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<210> 9
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<213> Artificial

<220>
<221> misc_feature
<222> (1)..(25)
<223> primer

<400> 9
gtgcgactgg cacaaggaca aagag 25

<210> 10
<211> 23
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(23)
<223> primer

<400> 10
ggggatcgtc atcattcgct cct 23

<210> 11
<211> 15
<212> PRT
<213> Artificial

<220>
<221> MISC_FEATURE
<222> (1)..(15)
<223> oligopeptide corresponding to C-terminus of CT120 protein

<400> 11

Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys
1          5          10          15

<210> 12
<211> 20
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(20)
<223> primer

<400> 12
atgctgctga cgctggccgg 20

<210> 13
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<213> Artificial

<220>

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<222> (1)..(20)

<223> primer

<400> 13

ttagccatcc tttttggctt

20

<210> 14

<211> 224

<212> PRT

<213> Homo sapiens

<400> 14

Met Ala Ser Thr Ala Gly Tyr Ile Val Ser Thr Ser Cys Lys His Ile
1 5 10 15
Ile Asp Asp Gln His Trp Leu Ser Ser Ala Tyr Thr Gln Phe Ala Val
20 25 30
Pro Tyr Phe Ile Tyr Asp Ile Tyr Ala Met Phe Leu Cys His Trp His
35 40 45
Lys His Gln Val Lys Gly His Gly Gly Asp Asp Gly Ala Ala Arg Ala
50 55 60
Pro Gly Ser Thr Trp Ala Ile Ala Arg Gly Tyr Leu His Lys Glu Phe
65 70 75 80
Leu Met Val Leu His His Ala Ala Met Val Leu Val Cys Phe Pro Leu
85 90 95
Ser Val Val Trp Arg Gln Gly Lys Gly Asp Phe Phe Leu Gly Cys Met
100 105 110
Leu Met Ala Glu Val Ser Thr Pro Phe Val Cys Leu Gly Lys Ile Leu
115 120 125
Ile Gln Tyr Lys Gln Gln His Thr Leu Leu His Lys Val Asn Gly Ala
130 135 140
Leu Met Leu Leu Ser Phe Leu Cys Cys Arg Val Leu Leu Phe Pro Tyr
145 150 155 160
Leu Tyr Trp Ala Tyr Gly Arg His Ala Gly Leu Pro Leu Leu Ala Val
165 170 175
Pro Leu Ala Ile Pro Ala His Val Asn Leu Gly Ala Ala Leu Leu Leu
180 185 190
Ala Pro Gln Leu Tyr Trp Phe Phe Leu Ile Cys Arg Gly Ala Cys Arg
195 200 205
Leu Phe Trp Pro Arg Ser Arg Pro Pro Pro Ala Cys Gln Ala Gln Asp
210 215 220

<210> 15

<211> 275

<212> PRT

<213> Homo sapiens

<400> 15

Met Leu Thr Pro Met Val Ala Gly Gly Val Val Phe Pro Gly Leu Phe
1 5 10 15
Leu Leu Ser Lys Asn Thr Leu Gln Arg Leu Pro Gln Leu Arg Trp Glu

20					25					30						
Glu	Ala	Asp	Ala	Val	Ile	Val	Ser	Ala	Arg	Leu	Val	Ser	Ser	Val	Gln	
35					40					45						
Ala	Ile	Met	Ala	Ser	Thr	Ala	Gly	Tyr	Ile	Val	Ser	Thr	Ser	Cys	Lys	
50					55					60						
His	Ile	Ile	Asp	Asp	Gln	His	Trp	Leu	Ser	Ser	Ala	Tyr	Thr	Gln	Phe	
65					70					75					80	
Ala	Val	Pro	Tyr	Phe	Ile	Tyr	Asp	Ile	Tyr	Ala	Met	Phe	Leu	Cys	His	
85					90					95						
Trp	His	Lys	His	Gln	Val	Lys	Gly	His	Gly	Gly	Glu	Asp	Gly	Thr	Pro	
100					105					110						
Arg	Ala	Leu	Gly	Ser	Thr	Trp	Ala	Val	Val	Arg	Gly	Tyr	Leu	His	Lys	
115					120					125						
Glu	Phe	Leu	Met	Val	Leu	His	His	Ala	Ala	Met	Val	Leu	Val	Cys	Phe	
130					135					140						
Pro	Leu	Ser	Val	Val	Trp	Arg	Gln	Gly	Lys	Gly	Asp	Phe	Phe	Leu	Gly	
145					150					155					160	
Cys	Met	Leu	Met	Ala	Glu	Val	Ser	Thr	Pro	Phe	Val	Cys	Leu	Gly	Lys	
165					170					175						
Ile	Leu	Ile	Gln	Tyr	Lys	Gln	Gln	His	Thr	Leu	Leu	His	Lys	Val	Asn	
180					185					190						
Gly	Ala	Leu	Met	Leu	Leu	Ser	Phe	Leu	Cys	Cys	Arg	Val	Leu	Leu	Phe	
195					200					205						
Pro	Tyr	Leu	Tyr	Trp	Ala	Tyr	Gly	Arg	His	Ala	Gly	Leu	Pro	Leu	Leu	
210					215					220						
Ser	Val	Pro	Met	Ala	Ile	Pro	Ala	His	Val	Asn	Leu	Gly	Ala	Ala	Leu	
225					230					235					240	
Leu	Leu	Ala	Pro	Gln	Leu	Tyr	Trp	Phe	Phe	Leu	Ile	Cys	Arg	Gly	Ala	
245					250					255						
Cys	Arg	Leu	Phe	Arg	Pro	Arg	Gly	Ser	Pro	Pro	Pro	Ser	Pro	Cys	Gln	
260					265					270						
Thr	Gln	Asp														
275																

<210> 16
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 16

Leu	Ala	Ile	Pro	Ser	Ser	Pro	Pro	Thr	Pro	Ser	Leu	Asn	Leu	Ala	Phe	
1	5				10				15							
Leu	Ser	Leu	Leu	Asp	Pro	Leu	Val	Ser	Leu	Pro	Gly	Phe	Lys	Ser	Pro	
20				25				30								
Cys	Leu	Pro	Gln	Trp	Trp	Leu	Gly	Gly	Trp	Cys	Ser	Pro	Asp	Ser	Ser	
35				40				45								
Ser	Tyr	Pro	Arg	Thr	Arg	Ser	Arg	Gly	Cys	Pro	Ser	Cys	Ala	Gly	Arg	
50				55				60								
Glu	Ala	Asp	Ala	Val	Ile	Val	Ser	Ala	Arg	Leu	Val	Ser	Ser	Val	Gln	
65					70					75					80	
Ala	Ile	Met	Ala	Ser	Thr	Ala	Gly	Tyr	Ile	Val	Ser	Thr	Ser	Cys	Lys	
85					90					95						
His	Ile	Ile	Asp	Asp	Gln	His	Trp	Leu	Ser	Ser	Ala	Tyr	Thr	Gln	Phe	
100					105					110						
Ala	Val	Pro	Tyr	Phe	Ile	Tyr	Asp	Ile	Tyr	Ala	Met	Phe	Leu	Cys	His	
115					120					125						

Trp	His	Lys	His	Gln	Val	Lys	Gly	His	Gly	Gly	Glu	Asp	Gly	Thr	Pro
130						135					140				
Arg	Ala	Leu	Gly	Ser	Thr	Trp	Ala	Val	Val	Arg	Gly	Tyr	Leu	His	Lys
145					150					155					160
Glu	Phe	Leu	Met	Val	Leu	His	His	Ala	Ala	Met	Val	Leu	Val	Cys	Phe
				165					170					175	
Pro	Leu	Ser	Val	Val	Trp	Arg	Gln	Gly	Lys	Gly	Asp	Phe	Phe	Leu	Gly
			180					185					190		
Cys	Met	Leu	Met	Ala	Glu	Val	Ser	Thr	Pro	Phe	Val	Cys	Leu	Gly	Lys
	195						200					205			
Ile	Leu	Ile	Gln	Tyr	Lys	Gln	Gln	His	Thr	Leu	Leu	His	Lys	Val	